

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 16, 2005, 21:10:15 ; Search time 147.538 Seconds
(Without alignment) 1436.539 Million cell updates/sec

Title: US-10-017-168-20

Perfect score: 2795

Sequence: 1 MFRSDMPKNTAIVEISNL.....AVLENFORFGFKDAFLKKAR 548

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseq19908:*

2: geneseq20008:*

3: geneseq20018:*

4: geneseq20028:*

5: geneseq20038:*

6: geneseq20048:*

7: geneseq20048:*

8: geneseq20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description	RESULT 1
1	2178	77.9	432	AAB43116	AB483116
2	1479	52.9	312	AAB43118	ID AAB483116 Standard; protein; 432 AA.
3	1043	37.3	232	AAB43117	XX
4	10.0	2768	4	AAB63397	AC AAB43116;
5	271	9.7	783	2	XX
6	269	9.6	567	4	DT 11-SEP-2003 (revised)
7	268.5	9.6	1000	ABJ25647	DT 20-APR-2001 (first entry)
8	259	9.3	522	4	XX
9	257	9.2	412	2	XX
10	250	8.9	902	4	XX
11	250	8.9	1018	2	XX
12	250	8.9	1018	2	XX
13	250	8.9	1018	4	XX
14	250	8.9	1018	8	XX
15	248	8.7	360	4	XX
16	242	8.7	34350	8	XX
17	236.5	8.5	2109	8	XX
18	232.5	8.3	7	ADN23693	XX
19	228	8.2	1388	6	XX
20	226	8.1	553	7	XX
21	224	8.0	1388	7	XX
22	223	8.0	489	4	XX
23	223	8.0	845	6	XX
24	222	7.9	864	4	XX
25	220.5	7.9	AAB23036	5	XX

ALIGNMENTS

26	217	7.8	611	2	AAI29039	AAI29039 T. gondii
27	217	7.8	611	4	AAU5510	AAU25510 T. gondii
28	217	7.8	611	7	ADG17131	ADG17131 T. gondii
29	217	7.8	679	4	AB59691	AB59691 Drosophili
30	216	7.7	1501	5	AAU76762	AAU76762 Plasmodiu
31	216	7.7	1568	7	ABP0152	ABP0152 Amino aci
32	213.5	7.6	382	4	AAB02399	AAB02399 Canine re
33	213	7.6	4412	3	AYY23666	AYY23666 Sequence
34	211	7.5	3551	8	AD00106	AD00106 Mouse hom
35	210	7.5	1192	4	ABBS9642	AB59642 Drosophil
36	210	7.5	1965	8	ADK7314	ADK7314 Streptoco
37	210	7.5	1972	8	ADP4616	ADP4616 Novel S.
38	208.5	7.5	293	4	ABE0398	ABE0398 Canine re
39	206.5	7.4	474	8	ADN4475	ADN4475 Thermococ
40	205	7.4	869	7	AD160170	AD160170 Secreted
41	205	7.3	385	6	ABU20070	ABU20070 Protein e
42	204	7.3	1026	4	AAM8825	Aam78825 Human pro
43	203	7.3	1245	5	ABP56885	ABP56885 Staphyloc
44	203	7.3	2397	6	ABU43308	ABU43308 Protein e
45	201	7.2	897	4	AAU37176	AAU37176 Staphyloc

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 OM protein - protein search, using SW model
 Run on: March 16, 2005, 21:14:51 ; Search time 31.1136 Seconds
 (without alignments)
 1694.657 Million cell updates/sec

SUMMARIES

ALIGNMENT

Q 394 hypothetical protein Tp0434 - syphilis spirochete
Q 395 Treponema pallidum subsp. pallidum [syphilis spirochete]
C; Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_charge 09-Jul-2004
C; Accession: G71326
C; Fraser, C.M.; Norris, S.J.; Weisstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Utterback, T.; McDaniel, K.; Kholak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A; Title: Complete genome sequence of *Treponema pallidum*, the syphilis spirochete.
A; Reference: Av1250; MUID:98332770; PMID:9665876
A; Accession: G71326
A; Status: preliminary; nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-227 <COL>
A; Cross-references: UNIPROT:08349; GB:AS001220; GB:AE000520; NID:93322705; PIDN: AAC654
A; Experimental source: strain Nichols
C; Genetics:
A; Gene: TP0434

Query Match
Best local **S**imilarity 39.0%; **S**core 1091.5; **DB** 2; **L**ength 227;
Matches 213; **C**onservative 2; **M**ismatches 11; **I**ndels 1; **G**aps 1;
Qy 322 R E G G E R E V E D V P K V E P A S E R E G G E R E V E D V P K V E P A S E R E G G E R E V E D V P K V E P A S G 381
Db 2 R E G S V - W E T C R R V E P A S E R E G G E R E G G L P K V E P A S E R E G G E R E V E D V P K V E P A S G 60

Qy 382 H E G G E R E V E D V P G V E P A S G H E G G E R E V E A S O H T K P Q S H V S N A ? N O F R N P G E L P F T L P 441
Db 61 H E G G E R E V E D V P G V E P A S G H E G G E R E V E A S O H T K P Q S H V S N A ? N O F R N P G E L P F T L P 120

Qy 442 D L E S E I V V P E O K G R A M P Q V I P E G A P R G L Q P Q E Y Y V Q I A V F H D A I Q Q S I H R Y G E Y P 501
Db 121 D L S E S E I V V P E O K G R A M P Q V I P E G A P R G L Q P Q E Y Y V Q I A V F H D A I Q Q S I H R Y G E Y P 180

Qy 502 I A V Q D I H E G K V R T V C V G P V Q D E R G A V L E N F R G F K D A F L K A R 548
Db 181 I A V Q D I H E G K V R T V C V G P V Q D E R G A V L E N F R G F K D A F L K A R 227

GenCore version 5.1.6									
Copyright (c) 1993 - 2005 Compugen Ltd.									
OM protein - protein search, using bw model									
Run on: March 16, 2005, 21:13:20 ; Search time 139.007 seconds									
(without alignments) 2018.738 Million cell updates/sec									
Title: US-10-017-168-20	2796	Perfect score: 1	MFVRSDMPKNTAVEISNL...	AVLENFQRGFKDAFLKKAR	548	Sequence: 081811 raphanus sa	081811 magnetospir	081811 plasmoidium	081811 dictyosteli
Scoring table: BIOSUM62									
Searched: Gapop 10.0 , Gapext 0.5									
Total number of hits satisfying chosen parameters: 1612378									
Minimum DB seq length: 0	200000000	Maximum DB seq length: 200000000	Post-processing: Minimum Match 0%	Maximum Match 100%	Listing first 45 summaries	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	1: uniprot_sprot;*	2: uniprot_trembl;*	
Database : UniProt 03;*									
SUMMARIES									
Result No.	Score	Query	Match Length	DB ID	Description	Best Local Similarity	Score	DB	Length
1	2796	100.0	548	2	Q93CA4	100.0%	2796;	2;	548
2	2178	77.9	432	2	Q01553	90.5%	2178;	2;	432
3	2092	74.8	428	2	Q9ALIV	89.5%	2092;	2;	428
4	1895.5	67.9	393	2	Q93CA3	83.5%	1895.5;	2;	393
5	1656	59.2	348	2	Q0ALW7	75.0%	1656;	2;	348
6	1093.5	39.0	227	083449	Q93CA4	60.0%	1093.5;	2;	227
7	967	34.6	256	2	Q83448	50.0%	967;	2;	256
8	536	19.2	458	2	Q73NG7	40.0%	536;	2;	458
9	303.5	10.9	1112	2	Q63G96	30.0%	303.5;	2;	1112
10	301.5	10.8	1108	2	Q9ND10	25.0%	301.5;	2;	1108
11	296	10.6	5458	2	Q9U559	20.0%	296;	2;	5458
12	290.5	10.4	1110	0	Q91255	15.0%	290.5;	2;	1110
13	280	10.0	2768	2	Q9VC00	10.0%	280;	2;	2768
14	277.5	9.9	897	2	Q13098	9.0%	277.5;	2;	897
15	273	9.8	1271	2	Q25861	8.0%	273;	2;	1271
16	271.5	9.7	721	1	YCF2_OENPI	7.0%	271.5;	1;	721
17	271.5	9.7	1554	2	Q07RN1	6.0%	271.5;	2;	1554
18	271	9.7	843	2	Q6G1M0	5.0%	271;	2;	843
19	269	9.6	432	2	Q964C9	4.0%	269;	2;	432
20	269	9.6	567	2	Q9HD28	3.0%	269;	2;	567
21	269	9.6	3455	2	Q65M59	2.0%	269;	2;	3455
22	268.5	9.6	913	2	Q13099	1.0%	268.5;	2;	913
23	268.5	9.6	913	2	Q6DC00	0.0%	268.5;	2;	913
24	268.5	9.5	982	0	Q73CUB	0.0%	268.5;	0;	982
25	261.5	9.4	1394	1	QNG4_BOVIN	0.0%	261.5;	1;	1394
26	259	9.3	572	2	Q8MKF9	0.0%	259;	2;	572
27	259	9.3	1233	2	Q81J56	0.0%	259;	2;	1233
28	257	9.2	2	Q26893	0.0%	257;	2;	2	
29	256.5	9.2	248	2	Q9LRH2	0.0%	256.5;	2;	248
30	256	9.2	466	2	Q6NB62	0.0%	256;	2;	466
31	256	9.2	5507	2	Q81HN3	0.0%	256;	2;	5507

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Om protein - protein search, using sw model

Run on: March 16, 2005, 21:10:15 ; Search time 84 Seconds

(without alignments) 1436.539 Million cell updates/sec

Title: US-10-017-168-6

Perfect score: 1572

Sequence: 1 MFTVRSMDMPKNTAVELNSLVE.....HTKOPSHSVNSNSAPNQFRKP 312

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16sec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003s:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match length	DB ID	Description
1	1572	100.0	312	4 AAB48618	Aab48318 T. pallid
2	1480	94.1	432	4 AAB48316	Aab48316 T. pallid
3	1118	71.1	232	4 AAB48317	Aab48317 T. pallid
4	214.5	13.6	1018	2 AAR98747	Aar98747 P. vivax
5	214.5	13.6	1018	2 AAR97039	Aar97039 A. secreta
6	214.5	13.6	1018	4 AAG66528	Aag66528 Plasmodium
7	214.5	13.6	1018	8 ADJ95471	Adj95471 Plasmodium
8	187.5	11.9	2109	8 ADN23693	Adn23693 Bacteriophage
9	187.5	11.9	2768	4 ABB63197	Abb63197 Drosophila
10	183	11.6	783	2 AAR05804	Aar05804 C-termina
11	179	11.4	552	7 ADC31182	Adc31182 Human nov
12	171	10.9	194	4 ABG11265	Abg11265 Novel hum
13	167.5	10.7	1000	5 ABJ25647	Abj25647 Aspergill
14	159	10.1	258	2 AAW55107	Aaw55107 Streptococ
15	159	10.1	258	5 ABP54601	Abp54601 S. pneumo
16	159	10.1	258	7 ADC5171	Adc5171 S. pneumo
17	159	10.1	553	7 ADM05820	Adm05820 Human pro
18	159	10.1	565	2 AAW61247	AAw61247 Streptococ
19	159	10.1	565	5 ABP54665	Abp54665 S. pneumo
20	159	10.1	565	7 ADC5299	Adc5299
21	159	10.1	1881	3 AAY4506	Aay4506
22	159	10.1	1881	6 ABU01047	Abu01047 S. pneumo
23	159	10.1	1881	8 ADM2119	Adm2119 S. pneumo
24	157.5	10.0	591	5 ABB2325	Abb2325 Herbicida
25	156.5	10.0	522	4 AAE02397	Aae02397 Canine re

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

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4: geneseqp2001s:*

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Post-processing: Minimum Match 0%

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Minimum DB seq length: 0

Maximum DB seq length: 200000000

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Om protein - protein search, using sw model

Run on: March 16, 2005, 21:14:51 ; Search time 17.7143 Seconds
 (Without alignment) 1694.657 Million cell updates/sec

Title: US-10-017-168-6
 Perfect score: 1572
 Sequence: 1 MFVRSDFMPPONTAVIEISNLRL... HTKQPSHSVSNSAPNQRRKP 312
 Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : PIR-79;*
 1: pir1;*
 2: pir2;*
 3: pir3;*
 4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	963	61.3	256	2	FP1326
2	430.5	27.4	227	2	GI1326
3	198	22.6	721	2	SG9795
4	195	12.4	407	1	BBB03
5	187.5	11.9	2109	2	BB9066
6	187.5	11.9	2109	2	TP3247
7	187	11.9	630	2	S29796
8	185	11.8	1271	2	AM5555
9	176	11.2	913	2	TP2485
10	175	11.1	391	2	S27850
11	174	11.1	450	2	CD9413
12	166.5	10.6	1094	2	S49313
13	165.5	10.5	590	2	A40437
14	162	10.3	1110	2	TP1116
15	159	10.1	1881	2	HP5076
16	157	10.0	1621	2	A82255
17	156.5	10.0	296	2	A54527
18	153.5	9.8	849	2	S00030
19	153	9.7	518	2	GG4488
20	151.5	9.6	1020	1	QPHUH
21	151.5	9.6	1076	2	TP6831
22	151	9.6	845	2	A45669
23	150	9.6	798	2	TP3022
24	150	9.5	679	2	S08366
25	148	9.4	1963	2	BP8002
26	145.5	9.3	506	2	TP4349
27	145.5	9.3	5170	2	TP15348
28	145	9.2	644	2	S55395
29	837	2	TP2761		

hypothetical protein
 immunoglobulin Al
 elastic titin - hu
 hypothetical prote
 hypothetical prote
 involucrin L - dou
 junctional sarcopl
 omega-conotoxin-se
 cell surface antig
 hypothetical prote
 protein T23E7.2b
 neurofilament trip
 antigen (C-termina
 Cmpy family prote
 hypothetical prote
 neurofilament trip

ALIGNMENTS

RESULT 1

Query Match 61.3%; Score 963; DB 2; Length 256;

Best Local Similarity 98.5%; Pred. No. 9.1e-51; Mismatches 3; Indels 0; Gaps 0;

Matches 192; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MFVRSDFMPPONTAVIEISNLRL... HTKQPSHSVSNSAPNQRRKP 312

DB 57 MFVRSDFMPPONTAVIEISNLRL... HTKQPSHSVSNSAPNQRRKP 312

QY 61 RVRTGTTGKGSQSPQGLSLASLPSRVPARPQDPPSSPPAGHTVBYRDTVFDPR 120

DB 17 RVRTGTTGKGSQSPQGLSLASLPSRVPARPQDPLSSPPAGHTVBYRDTVFDPR 176

QY 121 LVSPLSEREVDPVKVEPASEREGGEREVDPVKVEPASEREGGEREVDPVKVEPAS 180

DB 177 LVSPLSEREVDPVKVEPASEREGGEREVDPVKVEPASEREGGEREVDPVKVEPAS 236

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

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A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

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C;Genetics:

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A;Molecule type: DNA

A;Residues: 1-256 <COL>

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C;Genetics:

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A;Molecule type: DNA

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C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

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A;Gene: TP0433

A;Molecule type: DNA

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A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

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A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

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A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-256 <COL>

A;Cross-references: UNIPROT:O83448; GB:AB001220; GB:AE000520; NID:93322705; PIDN: AAC654

A;Experimental source: strain Nichols

C;Genetics:

A;Gene: TP0433

A;Molecule type: DNA

A;Residues: 1-

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GenCore version 5.1.6

OM protein - protein search, using SW model

Run on: March 16, 2005, 21:13:20 ; Search time 79.1429 Seconds
(without alignments)

Sequence: 1 MVRSDMFPKNTAVEISNLE.....HTKOPSHSVNSNAPNQFRKP 312
2018.738 Million cell updates/sec

Title: Perfect score: US-10-017-16B-6
152

Scoring table: BLOSSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*,
2: uniprot_sprot:*,
1: uniprot_trembl:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES					
Result No.	Score	Query Match Length	DB ID	Description	
1	1567	99.7	428	2 Q9ALV6	Q9alv6 treponema I
2	1480	94.1	432	2 Q51953	Q51953 treponema I
3	1479	94.1	548	2 Q93CA4	Q93ca4 treponema I
4	1364.5	86.8	393	2 Q93CA3	Q93ca3 treponema I
5	1113	70.8	348	2 Q9ALV7	Q9alv7 treponema I
6	963	61.3	256	2 Q83448	Q83448 treponema I
7	430.5	22.7	2	2 Q83449	Q83449 treponema I
8	345.5	22.0	458	2 Q73NG7	Q73ng7 treponema I
9	244.5	15.6	432	2 Q964C9	Q964c9 encyphalitite bacillus
10	237.5	15.1	1112	2 Q63G96	Q63g96 encyphalitite bacillus
11	228.5	14.5	410	2 Q96214	Q96214 encyphalitite bacillus
12	215	13.7	1167	2 Q9SH94	Q9sh94 neurospora
13	211	13.4	466	2 Q9E600	Q9e600 magnetospirillum
14	208.5	13.3	1070	2 Q8LYT0	Q8lyt0 bacillus
15	201	13.1	5458	2 Q9U459	Q9u459 plasmoidium
16	202.5	12.9	394	2 Q964D0	Q964d0 encyphalitite bacillus
17	202.5	12.9	453	1 PTP1_E1NGHE	PTP1_E1NGHE
18	198	12.6	248	2 Q9LRH2	Q9lrh2 rapanus
19	198	12.6	721	1 YCP2_OENPI	Ycp2_oenophila
20	195	12.4	407	1 IE68_SHV21	IE68_shv21
21	190.5	12.1	614	2 Q94674	Q94674 plasmoidium
22	189.5	12.1	690	2 Q6PC82	Q6pc82 brachydorid
23	187.5	11.9	2768	2 Q9VC00	Q9vc00 drosophila
24	185	11.9	10578	2 Q9ISF5	Q9isf5 caenorhabditis
25	187.5	11.9	18519	2 Q8ISF6	Q8isf6 caenorhabditis
26	187.5	11.9	18534	2 Q8ISF7	Q8isf7 caenorhabditis
27	187	11.9	630	1 YCP2_OENPI	Ycp2_oenophila
28	186	11.8	982	2 Q6CGV5	Q6cgv5 yarrowia
29	185	11.8	1271	2 Q25860	Q25860 plasmoidium
30	182	11.6	1108	2 Q9D1D0	Q9d1d0 babesia big
31	181.5	11.5	1554	2 Q7RMX1	Q7rmx1 plasmoidium

ALIGNMENTS	
RESULT 1	
Q9ALV6	PRELIMINARY;
ID Q9ALV6	PRT; 428 AA.
AC Q9ALV6;	
DT 01-JUN-2001 (TREMBrel; 17, Created)	
DT 01-DEC-2001 (TREMBrel; 19, Last sequence update)	
DT 01-OCT-2002 (TREMBrel; 22, Last annotation update)	
DB Acidic repeat protein.	
Name=arp;	
GN	
OS Treponema pallidum subsp. endemicum.	
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.	
OX NCBI_TAXID=55436;	
RN [1]	
RP SEQUENCE FROM N.A.	
RC STRAIN=Bosnia;	
RA Liu H., Steiner B. M., Rodes B.;	
RL Submitted (SBP-2001) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AR342807; ARK0161.2; -;	
SEQUENCE 428 AA; 4710 MW; B14EDB07443933 CRC64;	
RN [2]	
RP SEQUENCE FROM N.A.	
RC STRAIN=Bosnia;	
RA Liu H., Steiner B. M., Rodes B.;	
RL Submitted (SBP-2001) to the EMBL/GenBank/DBJ databases.	
DR EMBL; AR342807; ARK0161.2; -;	
SEQUENCE 428 AA; 4710 MW; B14EDB07443933 CRC64;	
Query Match 99.7%; Score 1567; DB 2; Length 428;	
Best local Similarity 99.7%; Prod. No. 8.3e-19;	
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
Qy 1 MFRYSDMFKEKTAELNSLNEKNAQAVTIGHAGIPLGLVSLAPAAQOLIGIVYQAVR 50	
Dy 1 MFRYSDMFKEKTAELNSLNEKNAQAVTIGHAGIPLGLVSLAPAAQOLIGIVYQAVR 60.	
Db 61 RVRILGTGTRGGSGTSDGSLASLSPSRPARPAQDPLSPSPACETVBYRTDWFDDR 120	
Db 61 RVRILGTGTRGGSGTSDGSLASLSPSRPARPAQDPLSPSPACETVBYRTDWFDDR 120	
Qy 121 LVPPLSREVEDPVKVERPASEREGGEREVEDPVKVERPASEREGGEREVEDPVKVERPAS 180	
Dy 121 LVSFLSREVEDPVKVERPASEREGGEREVEDPVKVERPASEREGGEREVEDPVKVERPAS 180	
Qy 181 ERGGEREVEDPVKVERPASEREGGEREVEDPVKVERPASEREGGEREVEDPVKVERPAS 240	
Dy 181 ERGGEREVEDPVKVERPASEREGGEREVEDPVKVERPASEREGGEREVEDPVKVERPAS 240	
Qy 241 ERGGEREVEDPVKVERPASEREGGEREVEDPVKVERPASEREGGEREVEDPVKVERPAS 300	
Dy 241 ERGGEREVEDPVKVERPASEREGGEREVEDPVKVERPASEREGGEREVEDPVKVERPAS 300	
Qy 301 VNSNAPNQFRKP 312	
Dy 301 VNSNAPNQFRNP 312	

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OM protein - protein search, using Bw model

Run on: March 16, 2005, 21:10:15 ; Search time 62.4615 Seconds

(without alignments) 1416.539 Million cell updates/sec

Title: US-10-017-168-4
Perfect score: 1168
Sequence: MFVFRSDMFPKNTAVEISNL... HTKQPSHSVNSNSAPNQFRKP 232

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1168	100.0	232	4 AAB48317
2	1118	95.7	312	4 AAB48318
3	1048	89.7	432	4 AAB48316
4	138.5	11.9	1018	2 AAB98747
5	138.5	11.9	1018	2 AAW97039
6	138.5	11.9	1018	4 AAG66528
7	138.5	11.9	1018	8 ABD95471
8	137	11.7	25	4 AAB48324
9	124.5	10.7	2109	8 ABD2693
10	124.5	10.7	19938	6 ABB76681
11	124	10.6	25	4 AAB48323
12	122	10.4	676	4 ABG11370
13	122	10.4	676	4 ABG29412
14	122	10.4	676	4 ABG11395
15	121	10.4	26	4 ABB48326
16	121	10.4	2768	4 ABB68397
17	119.5	10.2	1991	6 ABB052986
18	119.5	10.2	2263	7 ABB70425
19	119.5	10.2	2296	8 ABB60280
20	119.5	10.2	2352	8 ABB60278
21	119.5	10.2	2752	8 ABB24102
22	117.5	10.1	540	6 ABB44276
23	117	10.0	278	2 AAW55109
24	117	10.0	278	5 ABB54603
25	117	10.0	278	7 ADC45175

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

ALIGNMENTS

26	117	10.0	571	2 AAW55064	Jaw55064 Streptoco
27	117	10.0	571	5 ABP54558	Jbp54558 S. pneumo
28	117	10.0	571	7 ADC45085	Jdc45085 S. pneumo
29	117	10.0	1963	6 ABU46054	Jbu46054 protein e
30	117	10.0	1955	2 AAW69165	Jaw69165 Streptoco
31	117	10.0	1965	8 ADR47114	Jdr47114 Streptoco
32	117	10.0	1972	8 ADR9416	Jdr9416 Novel S.
33	117	10.0	2004	6 ABU1577	Jbu01577 S. pneumo
34	117	10.0	2004	8 ADM92167	Jdm92167 S. pneumo
35	116	9.9	2 AAW55107	Jaw55107 Streptoco	
36	116	9.9	258	5 ABP54601	Jbp54601 S. pneumo
37	116	9.9	258	7 ADC45171	Jdc45171 S. pneumo
38	116	9.9	552	7 ADC31182	Jdc31182 Human nov
39	116	9.9	565	2 AAW61247	Jaw61247 Streptoco
40	116	9.9	565	4 ABP54665	Jbp54665 S. pneumo
41	116	9.9	565	7 ADC45299	Jdc45299 S. pneumo
42	116	9.9	1881	3 AAY4506	Jay4506 Streptoco
43	116	9.9	1881	6 ABU01047	Jbu01047 S. pneumo
44	116	9.9	1881	8 ADM92119	Jdm92119 S. pneumo
45	113	9.7	456	4 ABB58301	Jbb58301 Drosophil

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

RESULT 1

ID AAB48317 standard; protein; 232 AA.

XX

AC AAB48317;

XX

DT 11-SEP-2003 {revised}

DT 20-APR-2001 {first entry}

XX

T. pallidum ssp. pertenue (CDC-2) acidic repeat protein (arp).

XX

XX Treponeema pallidum; acidic repeat protein; arp; immunogenic; syphilis; yaws; bejel.

XX

OS Treponeema pallidum; ssp. pertenue.

XX

PR WO20077465-A2.

XX

PD 21-DBC-2000.

XX

PP 14-JUN-2000; 99US-013981P.

XX

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Liu H, Steiner B, Rhodes B;

XX

DR WPI: 2001-080711/09.

DR N-PSDB; AAC846464.

XX

Detected Treponeema pallidum in blood, saliva, etc., by detecting formation of a complex between immunogenic peptides of acidic repeat protein of the bacterium and an antibody present in the biological sample.

XX

Claim 15; Fig 8; 73pp; English.

The invention relates to a method of detecting presence of Treponeema pallidum (Tp), anti-Treponeema antibodies (Ab), or both in a biological sample that involves contacting an acidic repeat protein (arp), or one or more isolated immunogenic Tp peptides of arp with an Ab containing biological sample and then detecting the formation of a complex between immunogenic peptides and Ab. The presence of the complex indicates the presence of Tp. The method is thus useful for diagnosing syphilis, yaws, and bejel diseases. The immunogenic peptides or the Ab are raised against arp, as part of an immunogenic composition, are useful for inducing a protective immune response against syphilis, yaws or bejel caused by Tp.

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On protein - protein search, using sw model

Run on: March 16, 2005, 21:13:20 ; Search time 58.8498 Seconds
 (without alignments)
 2018.738 Million cell updates/sec

Title: US-10-017-168-4

Perfect score: 1168

Sequence: 1 MFVRSDMFPKNTAVEISNL.....HTKOPSHSVNSAPNQFRKP 232

Scoring table: BLOSUM62

Gapop 10.0 , gapext 0.5

Searched:

1612378 seqb, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot;*
 2: uniprot_trembl;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1163	99.6	348	2 Q9ALV7
2	1130.5	96.8	393	2 Q93CA3
3	1113	95.3	428	2 Q9ALV6
4	1048	89.7	432	2 Q91V53
5	1043	89.3	548	2 Q93CA4
6	963	82.4	256	2 Q93448
7	429	227	093449	treponema p
8	286	24.5	458	2 Q73NG7
9	162	13.9	410	2 Q96214
10	160	13.7	432	2 Q964C9
11	152.5	13.1	466	2 Q6NE60
12	147	12.6	394	2 Q964D0
13	147	12.6	453	1 PTP1_EENHE
14	146.5	12.5	1167	2 Q7SH94
15	144.5	12.4	1070	2 Q81Y70
16	144	12.3	1112	2 Q63G95
17	133.5	11.4	891	2 Q6NVTO
18	129	11.0	675	2 Q871R0
19	126.5	10.8	614	2 Q94674
20	125.5	10.7	519	2 Q7S118
21	125.5	10.7	915	2 Q6PMB
22	124.5	10.7	10578	2 Q81SP5
23	124.5	10.7	18519	2 Q81SF6
24	124.5	10.7	18534	2 Q81SF7
25	123.5	10.6	796	2 Q96579
26	122	10.4	1942	2 Q7NAY2
27	121.5	10.4	690	2 Q6PC82
28	121	10.4	687	2 Q7S73
29	121	10.4	2768	2 Q9VC00
30	120	10.3	1754	2 Q80U37
31	120	10.3	2607	2 Q8BT8

RESULT 1		ALIGNMENTS	
ID	Q9ALV7	PRELIMINARY;	PRT; 348 AA.
AC	Q9ALV7;		
DT	01-JUN-2001 (TREMBrel. 17, Created)		
DT	01-DEC-2001 (TREMBrel. 19, Last sequence update)		
DR	01-OCT-2002 (TREMBrel. 22, Last annotation update)		
GN	Name=arp;		
OS	Treponema pallidum (subsp. pertenue) (Yaws treponeme), Bacterium; Spirochaetes; Spirochaetales; Treponema.		
OC	OX NCBI_TaxID=168;		
RN	[1]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[2]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[3]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[4]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[5]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[6]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[7]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[8]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[9]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[10]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[11]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[12]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[13]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[14]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[15]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[16]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[17]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[18]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[19]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[20]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[21]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[22]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[23]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[24]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[25]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[26]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[27]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[28]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[29]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[30]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[31]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[32]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[33]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[34]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[35]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[36]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[37]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[38]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[39]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[40]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[41]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[42]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[43]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[44]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[45]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[46]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[47]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[48]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[49]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		
RL	Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.		
RN	[50]		
RR	SEQUENCE FROM N.A.		
RC	SEQUENCE FROM N.A.		
RA	Liu H., Steiner B.M.; Rodes B.;		

